

Query= SEQ ID NO:9 (PE029)
(184 letters)

Sequences producing significant alignments:

	Score (bits)	E Value
AL390242.17.1.68883	<u>192</u>	5e-47
AL158844.14.1.53402	<u>78</u>	8e-13

>AL390242.17.1.68883
Length = 68883

Score = 192 bits (97), Expect = 5e-47
Identities = 97/97 (100%)
Strand = Plus / Plus

Query: 88 agcacaccaacatggcacatgtatacatatgtAACAAACCTGcacattgtgcacatgtac 147
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 3247 agcacaccaacatggcacatgtatacatatgtAACAAACCTGcacattgtgcacatgtac 3306

Query: 148 cctaaaacttaaagtgtAACATAATAAAATTTTTT 184
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 3307 cctaaaacttaaagtgtAACATAATAAAATTTTTT 3343

>AL158844.14.1.53402
Length = 53402

Score = 77.8 bits (39), Expect = 8e-13
Identities = 45/48 (93%)
Strand = Plus / Plus

Query: 40 actgntttgcaagctgnntaagtggagcaatcttggaaagattca 87
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 53105 actgttgtttgcaagctggtaagtggagcaatcttggaaagattca 53152

Query= SEQ ID NO:10 (PE029)
(309 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AC087564 ACCESSION:AC087564 NID: gi 28933558 gb AC087564.6 Hom...	589	e-165
AC007344 ACCESSION:AC007344 NID: gi 5851724 gb AC007344.3 AC007...	589	e-165

>AC087564 ACCESSION:AC087564 NID: gi 28933558 gb AC087564.6 Homo sapiens
chromosome 16 clone RP11-437L7, complete sequence
Length = 157233

Score = 589 bits (297), Expect = e-165
Identities = 309/310 (99%), Gaps = 1/310 (0%)
Strand = Plus / Minus

Query: 1 ggaagcttcacaccacatttgttctgacaagagaaggagaaatcggtggcctctgc 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 105042 ggaagcttcacaccacatttgttctgacaagagaaggagaaatcggtggcctctgc 104983

Query: 61 gtgacatggagggtccccccacctgcaagctttgtttgtggatcttggacagtacc 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 104982 gtgacatggagggtccccccacctgcaagctttgtttgtggatcttggacagtacc, 104923

Query: 121 ctggcgaaaagcattcgcaagattatccggctagcacagcctcaagaataatatct 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 104922 ctggcgaaaagcattcgcaagattatccggctagcacagcctcaagaataatatct 104863

Query: 240 aaaaaaggctacaattcatatgcaaactagaggaggattccatgattcataataaaat 299
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 104802 aaaaaaggctacaattcatatgcaaactagaggaggattccatgattcataataaaat 104743

Query: 300 gttgaaacgc 309
||| | | | | | | |
Sbjct: 104742 qttqaaacqc 104733

>AC007344 ACCESSION:AC007344 NID: gi 5851724 gb AC007344.3 AC007344 Homo sapiens chromosome 16 clone RPCI-11_466G2, complete sequence
Length = 180827

Score = 589 bits (297), Expect = e-165
Identities = 309/310 (99%), Gaps = 1/310 (0%)
Strand = Plus / Plus

Query: 1 ggaagcttcacaccatttgttcctgacaagagaaggagaaatcggtggcctctgc 60
Sbjct: 176532 ggaagcttcacaccatttgttcctgacaagagaaggagaaatcggtggcctctgc 176591

Query: 61 gtgacatggagggtcccccacctgcaagctttgtgtttgctggatcttggacagtacc 120
Sbjct: 176592 gtgacatggagggtcccccacctgcaagctttgtgtttgctggatcttggacagtacc 176651

Query: 121 ctggcgaaaagcattcggcaagattatccggctagcacagccttcaaggaataaatct 180
Sbjct: 176652 ctggcgaaaagcattcggcaagattatccggctagcacagccttcaaggaataaatct 176711

Query: 181 aacaccttgttccc-tttgcggttcaaaagccactgtcactgggtacataggcagttt 239
Sbjct: 176712 aacaccttgttccctttgcgggtcaaaagccactgtcactgggtacataggcagttt 176771

Query: 240 aaaaaaggctacaattcatatgcaaactagaggaggattccatgattcataataaaat 299
Sbjct: 176772 aaaaaaggctacaattcatatgcaaactagaggaggattccatgattcataataaaat 176831

Query: 300 gttgaaacgc 309
Sbjct: 176832 gttgaaacgc 176841

Query= SEQ ID NO:11 (PE029)
(143 letters)

Score E
(bits) Value

Sequences producing significant alignments:

AC019129 ACCESSION:AC019129 NID: gi 16077059 gb AC019129.8 Hom... 266 1e-68

>AC019129 ACCESSION:AC019129 NID: gi 16077059 gb AC019129.8 Homo
sapiens BAC clone RP11-559M23 from 2, complete sequence
Length = 172611

Score = 266 bits (134), Expect = 1e-68
Identities = 140/143 (97%)
Strand = Plus / Minus

Query: 1 gtggccatgtacttggcttaaggtaaggattctactactgtngaaganggagagaacgg 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 94486 gtggccatgtacttggcttaaggtaaggattctactactgtagaagaaggagagaacgg 94427

Query: 61 nttctagaggacaactggcagtctcctttagctgagactttttgtgtataaaaattaa 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 94426 attctagaggacaactggcagtctcctttagctgagactttttgtgtataaaaattaa 94367

Query: 121 taaaattggtttatttaatttggtt 143
||| ||| ||| ||| ||| |||
Sbjct: 94366 taaaattggtttatttaatttggtt 94344

Query= SEQ ID NO:12 (PE029)
(210 letters)

Score E
(bits) Value

Sequences producing significant alignments:

AC016601.7.1.145264 281 8e-74
AC034246.4.1.155025 281 8e-74

>AC016601.7.1.145264
Length = 145264

Score = 281 bits (142), Expect = 8e-74
Identities = 146/147 (99%), Gaps = 1/147 (0%)
Strand = Plus / Minus

Query: 64 agagatggggtttcgcatgtgcccaggctggtctaagtcctgaactcaagtgatc 123
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 36474 agagat-ggggtttcgcatgtgcccaggctggtctaagtcctgaactcaagtgatc 36416

Query: 124 ttcccacctaagcctccaaagtgctggattacaggcatgagccacgactcccagcctg 183
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 36415 ttcccacctaagcctccaaagtgctggattacaggcatgagccacgactcccagcctg 36356

Query: 184 aaatatagatttaatcttcagcttgc 210
||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 36355 aaatatagatttaatcttcagcttgc 36329

Score = 129 bits (65), Expect = 7e-28
Identities = 65/65 (100%)
Strand = Plus / Minus

Query: 1 atctatgcagattagctctgccttccttaataactggactcttgagcatctgatt 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 43711 atctatgcagattagctctgccttccttaataactggactcttgagcatctgatt 43652

Query: 61 gacag 65
|||
Sbjct: 43651 gacag 43647

>AC034246.4.1.155025
Length = 155025

Score = 281 bits (142), Expect = 8e-74
Identities = 146/147 (99%), Gaps = 1/147 (0%)
Strand = Plus / Plus

Query: 64 agagatgggggttcgccatgtgccaggctggtctcaagctcctgaactcaagtgatc 123
Sbjct: 16092 agagat-ggggttcgccatgtgccaggctggtctcaagctcctgaactcaagtgatc 16150

Query: 124 ttcccacctaagcctccaaagtgctggattacaggcatgagccacgactcccagcctg 183
Sbjct: 16151 ttcccacctaagcctccaaagtgctggattacaggcatgagccacgactcccagcctg 16210

Query: 184 aaatatagatttaatcttcagcttgc 210
Sbjct: 16211 aaatatagatttaatcttcagcttgc 16237

Score = 129 bits (65), Expect = 7e-28
Identities = 65/65 (100%)
Strand = Plus / Plus

Query: 1 atctatgcagattagctctgccttccttaataactggactcttggagcatctgatt 60
Sbjct: 8857 atctatgcagattagctctgccttccttaataactggactcttggagcatctgatt 8916

Query: 61 gacag 65
Sbjct: 8917 gacag 8921

Query= SEQ ID NO:13 (PE029)
(453 letters)

Score E
Sequences producing significant alignments: (bits) Value

AL391500 ACCESSION:AL391500 NID: gi 12227422 emb AL391500.13 H... 735 0.0

>AL391500 ACCESSION:AL391500 NID: gi 12227422 emb AL391500.13 Human DNA
sequence from clone RP11-707M13 on chromosome 6, complete
sequence
Length = 171220

Score = 735 bits (371), Expect = 0.0
Identities = 371/371 (100%)
Strand = Plus / Minus

Query: 1 gtatacatccagatggccgaaagcaactgaagatccacaaaagaagtgaaaatagccgta 60
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 76957 gtatacatccagatggccgaaagcaactgaagatccacaaaagaagtgaaaatagccgta 76898

Query: 61 actgatgacattccaccattgtgatttgttctgccccaccgtaactgatcaatgtactt 120
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 76897 actgatgacattccaccattgtgatttgttctgccccaccgtaactgatcaatgtactt 76838

Query: 121 tgtaatctccccacccttaagaaggttttgtaatctccccacccttaagaatgttc 180
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 76837 tgtaatctccccacccttaagaaggttttgtaatctccccacccttaagaatgttc 76778

Query: 181 tttgttaattctccccacccttgagaatgtactttgtgagatctaccctgcccacaaaa 240
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 76777 tttgttaattctccccacccttgagaatgtactttgtgagatctaccctgcccacaaaa 76718

Query: 241 cattggcctgactccaccgcctatccaaaacctataagaactaatgataatccacca 300
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 76717 cattggcctgactccaccgcctatccaaaacctataagaactaatgataatccacca 76658

Query: 301 ccctttgctgactctttcggactcagccgcctgcaccaggtaaaacacgcct 360
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 76657 ccctttgctgactctttcggactcagccgcctgcaccaggtaaaacacgcct 76598

Query: 361 tggtgctcaca 371
||| |||||
Sbjct: 76597 tggtgctcaca 76587

Query= SEQ ID NO:14 (PE029)
(344 letters)

Score E
(bits) Value

Sequences producing significant alignments:

AL354814.19.1.70126	<u>281</u>	1e-73
AL391683.8.1.168373	<u>238</u>	2e-60
AL160397.17.1.204056	<u>163</u>	2e-38

>AL354814.19.1.70126
Length = 70126

Score = 281 bits (142), Expect = 1e-73
Identities = 145/146 (99%)
Strand = Plus / Plus

Query: 199 caggaagaaaaatggaactaaaaaggaaaacaatagcaacaaagatcaaaataaataac 258
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 25129 caggaagaaaaatggaactaaaaaggaaaacaatagcaacaaagatcaaaataaataac 25188

Query: 259 aaggaagcggagagaagaaagaacatggtaagagagtgaaaagcattgtcattgggt 318
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 25189 aaggaagcggagagaagaaagaacatggtaagagagtgaaacgcattgtcattgggt 25248

Query: 319 gaattgcagaaagaataaattattg 344
||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 25249 gaattgcagaaagaataaattattg 25274

>AL391683.8.1.168373
Length = 168373

Score = 238 bits (120), Expect = 2e-60
Identities = 120/120 (100%)
Strand = Plus / Plus

Query: 83 aatttcgctttgttgcggcaggctggagtgcatacgagatcttggctcaactgcaacct 142
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 140792 aatttcgctttgttgcggcaggctggagtgcatacgagatcttggctcaactgcaacct 140851

Query: 143 ccaccccccagggttaagtgattctcctgcctcagcctcccaagtagctggattacagg 202
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 140852 ccaccccccagggttaagtgattctcctgcctcagcctcccaagtagctggattacagg 140911

>AL160397.17.1.204056
Length = 204056

Score = 163 bits (82), Expect = 2e-38
Identities = 82/82 (100%)
Strand = Plus / Plus

Query: 1 tgcctccagaaagaacgcagccctactgacacctgggtttggcctggtagagaccaactt 60
|||||||
Sbjct: 1502 tgcctccagaaagaacgcagccctactgacacctgggtttggcctggtagagaccaactt 1561

Query: 61 tggactttcacttccaaaact 82
|||||||
Sbjct: 1562 tggactttcacttccaaaact 1583

Query= SEQ ID NO:15 (PE029)
(473 letters)

Score E
(bits) Value

Sequences producing significant alignments:

AC084117 ACCESSION:AC084117 NID: gi 22165345 gb AC084117.6 Hom... 414 e-113

>AC084117 ACCESSION:AC084117 NID: gi 22165345 gb AC084117.6 Homo
sapiens chromosome 11, clone RP11-107C21, complete
sequence
Length = 166973

Score = 414 bits (209), Expect = e-113
Identities = 215/217 (99%)
Strand = Plus / Minus

Query: 192 caggtctacattctttgccatactgctctggctctgggggtgacctgaatggacc 251
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 84399 caggtctacattctttgccatactgctctggctctgggggtgacctgaatggacc 84340

Query: 252 acacagccatgggtctcctgtcctccaccttactggtaagactggagtgaggaaga 311
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 84339 acacagccatgggtctcctgtcctccaccttactggtaagactggagtgaggaaga 84280

Query: 312 agagtgagattgcaccctctgcaggaccatggcagaccctgcccattacctttctc 371
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 84279 agagtgagattgcaccctctgcaggaccatggcagaccctgcccattacctttctc 84220

Query: 372 aggggtctctttctcttattaaacttctttccatt 408
||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 84219 aggggtctctttctcttattaaacttctttccatt 84183

Query= SEQ ID NO:16 (PE029)
(403 letters)

Score E
(bits) Value

Sequences producing significant alignments:

AP003031.3.1.95585 456 e-126

>AP003031.3.1.95585
Length = 95585

Score = 456 bits (230), Expect = e-126
Identities = 240/243 (98%), Gaps = 1/243 (0%)
Strand = Plus / Minus

Query: 161 gagccaagaagtccctcaaaggatggaggaacacatgaatatacatt 220
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 27019 gagccaagaagtccctcaaaggatggaggaacacatgaatatacatt 26960

Query: 221 aaatcctccttccacagagactcactgaaggaaatgaagaaggaaaagtcccttaatt 280
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 26959 aaatcctccttccacagagactcactgaaggaaatgaagaaggaaaagtcccttaatt 26900

Query: 281 attaagatgcgttccggactcgagaaatttggaaaccccaagtcttgaatac 340
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 26899 attaagatgcgttccggactcgagaaatttggaaaccccaagtcttgaatac 26840

Query: 341 atttctctaaagaggccgaataacttaataatcagggagatataagcaatggagac-c 399
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 26839 atttctctaaagaggccgaataacttaataatcagggagatataagcaatggtagacac 26780

Query: 400 cct 402
|||
Sbjct: 26779 cct 26777

Score = 311 bits (157), Expect = 2e-82
Identities = 160/161 (99%)
Strand = Plus / Minus

Query: 1 gagtctactgacagaaggccaaagggttgcgttagttcagcttcgttgcatt 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 37882 gagtctactgacaaaaggccaaagggttgcgttagttcagcttcgttgcatt 37823

Query: 61 ttttcaaaaatgtctgactgcattttggacattataaaaaccacagtaggaaaaacg 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 37822 ttttcaaaaatgtctgactgcattttggacattataaaaaccacagtaggaaaaacg 37763

Query: 121 ccagctatttcaatggaccaacaaagtgagactccaaagtg 161
Sbjct: 37762 ccagctatttcaatggaccaacaaagtgagactccaaagtg 37722

Query= SEQ ID NO:17 (PE029)
(445 letters)

Score E
(bits) Value

Sequences producing significant alignments:

AL158141.14.1.184181 535 e-150

>AL158141.14.1.184181
Length = 184181

Score = 535 bits (270), Expect = e-150
Identities = 312/329 (94%), Gaps = 2/329 (0%)
Strand = Plus / Plus

Query: 118 agggtctgctctgtcgcccaggctagagtgcagtgccgcaatcttggctatggcaacc 177
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 9434 agggtctgctctgtcgcccaggctagagtgcagtgccgcaatcttggctatggcaacc 9493

Query: 178 tccaccccccgggtcaagcgattctcctgccacagcctccgagtagctgggattacag 237
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 9494 tccaccccccgggtcaagcgattctcctgccacagcctccgagtagctgggattacag 9553

Query: 238 gtgcctaccaccaggcccagctaaatttttgtattttagacagacggggttcgcc 297
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 9554 gtgcctaccaccaggcccagctaaatttttgtattttagacagacggggttcgcc 9613

Query: 298 accttggccaggctggcttgaactcctgaccttgcattctacccacnntccaa 357
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 9614 accttggccaggctggcttgaactcctgaccttgcattctacccacnntccaa 9673

Query: 358 ngggctggnattacagggggagagacccgacccagccaccttactgngttctgantgn 417
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 9674 agtgctgggattacaggtgtgagagacccgacccagccaccttactgagttctgattgc 9733

Query: 418 nnttccttcct-ttcctttcccttaa 445
||| ||| ||| ||| ||| ||| |||
Sbjct: 9734 tcttcctt-cctttcccttccttaa 9761

Score = 238 bits (120), Expect = 2e-60
Identities = 120/120 (100%)
Strand = Plus / Plus

Query: 1 agacgggggtctcactacgttggccaggctgatcttgaactcctgcctcaaattgaccctc 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 8124 agacgggggtctcactacgttggccaggctgatcttgaactcctgcctcaaattgaccctc 8183

Query: 61 ctgcctcagcctccaaagtgcgtcgatataaggcacaaggccactgtgccaaccaaagg 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 8184 ctgcctcagcctccaaagtgcgtcgatataaggcacaaggccactgtgccaaccaaagg 8243

Query= SEQ ID NO:18 (PE029)
(486 letters)

Score E
(bits) Value
Sequences producing significant alignments:

AL158141.14.1.184181 599 e-169

>AL158141.14.1.184181
Length = 184181

Score = 599 bits (302), Expect = e-169
Identities = 347/362 (95%), Gaps = 3/362 (0%)
Strand = Plus / Plus

Query: 118 agggtctgctctgtcgcccaggctagagtgcagtgccgcaatcttggctatggcaacc 177
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 9434 agggtctgctctgtcgcccaggctagagtgcagtgccgcaatcttggctatggcaacc 9493

Query: 178 tccaccccccgggtcaagcgattctcctgccacagcctcccgagtagctgggattacag 237
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 9494 tccaccccccgggtcaagcgattctcctgccacagcctcccgagtagctgggattacag 9553

Query: 238 gtgcctaccaccaggcccagct-aattttttgtattttagtacagacggggttcgcc 296
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 9554 gtgcctaccaccaggcccagctaaattttttgtattttagtacagacggggttcgcc 9613

Query: 297 accttggccaggctggcttgaactcctgaccttgcgtatctacccacctcagtctccaa 356
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 9614 accttggccaggctggcttgaactcctgaccttgcgtatctacccacctcagtctccaa 9673

Query: 357 agtgctgggattacagggtgtgagagacccgacccaggcaccttactgaggttctgaatgn 416
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 9674 agtgctgggattacagggtgtgagagacccgacccaggcaccttactgagttctgattgc 9733

Query: 417 tctttcncntttttccctttccctaaattggccaaagttnatcctggctttt 476
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 9734 tctttcc-ttcctttcccttct-cccttaacttgcccaaagtttatccttgactttt 9791

Query: 477 tt 478
||
Sbjct: 9792 tt 9793

Score = 238 bits (120), Expect = 3e-60
Identities = 120/120 (100%)
Strand = Plus / Plus

```
Query: 61  ctgcctcagcctccaaagtgtcgattaaaggcacaagccactgtgcccaccaaagg 120
          ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||| |
Sbjct: 8184 ctgcctcagcctccaaagtgtcgattaaaggcacaagccactgtgcccaccaaagg 8243
```